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Search Request

Examiner's Name:	David Lambertson
Examiner #:	79514
Art Unit:	1636
Room #:	12D06
Mailbox room#:	11E12
Phone:	(703) 308-8365
Results Format:	paper

Serial #:09/757049

Please Search:

Nucleic Acid databases for:

SEQ ID No: 13, 15, 21, 22 and 27

Including:

1. Interference Search Only.

These sequences are primers, 12-15 nucleotides in length, so I didn't think special permission was required. Please let me know if this is otherwise.

Thanks,
Dave.

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Transcription Factor Binding Site Search

TFSEARCH Search Result

** TFSEARCH ver.1.3 ** (c)1995 Yutaka Akiyama (Kyoto Univ.)

This simple routine searches highly correlated sequence fragments
versus TFMATRIX transcription factor binding site profile database
by E.Wingender, R.Knueppel, P.Dietze, H.Karas (GBF-Braunschweig).

<Warning> Scoring scheme is so straightforward in this version.
score = 100.0 * ('weighted sum' - min) / (max - min)
The score does not properly reflect statistical significance!

Database: TRANSFAC MATRIX TABLE, Rel.3.3 06-01-1998
Query: untitled (9 bases)
Taxonomy: ALL
Threshold: 85.0 point

TFMATRIX entries with High-scoring:

		entry	score
1	TTAACATAA		

Total 0 high-scoring sites found.

** No TFMATRIX entry hit for your sequence. **

- **TRANSFAC** database document (Notice to users)
- **TFMATRIX:** binding site distribution matrix

- **Parallel Application Tsukuba Laboratory** Home Page
- **PAPIA system** Top Page

TFSEARCH Search Result

```
** TFSEARCH  ver.1.3 **   (c)1995 Yutaka Akiyama (Kyoto Univ.)

 This simple routine searches highly correlated sequence fragments
 versus TFMATRIX transcription factor binding site profile database
 by E.Wingender, R.Knueppel, P.Dietze, H.Karas (GBF-Braunschweig).

  <Warning> Scoring scheme is so straightforward in this version.
            score = 100.0 * ('weighted sum' - min) / (max - min)
            The score does not properly reflect statistical significance!

 Database:  TRANSFAC MATRIX TABLE, Rel.3.3 06-01-1998
 Query:     untitled (12 bases)
 Taxonomy:  ALL
 Threshold: 85.0 point

 TFMATRIX entries with High-scoring:

   1 GATTTACCAT AA                                          entry        score


 Total 0 high-scoring sites found.

** No TFMATRIX entry hit for your sequence. **
```

- **TRANSFAC** database document (Notice to users)
- **TFMATRIX:** binding site distribution matrix

- **Parallel Application Tsukuba Laboratory** Home Page
- **PAPIA system** Top Page

TFSEARCH Search Result

```
** TFSEARCH  ver.1.3 **   (c)1995 Yutaka Akiyama (Kyoto Univ.)

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 by E.Wingender, R.Knueppel, P.Dietze, H.Karas (GBF-Braunschweig).

  <Warning> Scoring scheme is so straightforward in this version.
            score = 100.0 * ('weighted sum' - min) / (max - min)
            The score does not properly reflect statistical significance!

 Database:  TRANSFAC MATRIX TABLE, Rel.3.3 06-01-1998
 Query:     untitled (16 bases)
 Taxonomy:  ALL
 Threshold: 85.0 point


 TFMATRIX entries with High-scoring:

   1 AATAAAATCA AAAATT
          ------->
             <-------

                                                  entry          score
                                                  M00148 SRY      90.9
                                                  M00100 CdxA     87.2


 Total 2 high-scoring sites found.
 Max score: 90.9 point, Min score: 87.2 point
```

- **TRANSFAC** database document (Notice to users)
- **TFMATRIX:** binding site distribution matrix

- **Parallel Application Tsukuba Laboratory** Home Page
- **PAPIA system** Top Page

TFSEARCH Search Result

** TFSEARCH ver.1.3 ** (c)1995 Yutaka Akiyama (Kyoto Univ.)

This simple routine searches highly correlated sequence fragments
versus TFMATRIX transcription factor binding site profile database
by E.Wingender, R.Knueppel, P.Dietze, H.Karas (GBF-Braunschweig).

<Warning> Scoring scheme is so straightforward in this version.
score = 100.0 * ('weighted sum' - min) / (max - min)
The score does not properly reflect statistical significance!

Database: TRANSFAC MATRIX TABLE, Rel.3.3 06-01-1998
Query: untitled (15 bases)
Taxonomy: ALL
Threshold: 85.0 point

TFMATRIX entries with High-scoring:

```
  1 AAAGGGGAAC ACTTT
        ---->
   ------->
     ----->
   ------->
```

entry		score
M00029	HSF	90.9
M00154	STRE	89.6
M00048	ADR1	89.2
M00083	MZF1	88.7

Total 4 high-scoring sites found.
Max score: 90.9 point, Min score: 88.7 point

- **TRANSFAC** database document (Notice to users)
- **TFMATRIX:** binding site distribution matrix

- **Parallel Application Tsukuba Laboratory** Home Page
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Promoters

From E. Coli

Genname	ECD AccNr	map position	Sequence source	(start-end)	Contig	C
agaY	CO05664	70.69	U18997	(63895-64755)	ECD065.00	-
CP05102	CP05102	92.85	U14003	(2010-1983)	ECD090.00	-
CP05103	CP05103	92.89	U14003	(3979-3952)	ECD090.00	-
CP05104	CP05104	93.16	U14003	(16362-16335)	ECD090.00	-
CP05105	CP05105	93.16	U14003	(16742-16713)	ECD090.00	-
CP05106	CP05106	93.18	U14003	(17659-17631)	ECD090.00	-
CP05107	CP05107	93.19	U14003	(17695-17724)	ECD090.00	-
CP05108	CP05108	93.26	U14003	(21114-21142)	ECD090.00	-
CP05109	CP05109	93.33	U14003	(24224-24196)	ECD090.00	-
CP05110	CP05110	93.40	U14003	(27865-27840)	ECD090.00	-
CP05111	CP05111	93.43	U14003	(28905-28876)	ECD090.00	-
CP05112	CP05112	93.48	U14003	(31418-31390)	ECD090.00	-
CP05113	CP05113	93.59	U14003	(36386-36358)	ECD090.00	-
CP05114	CP05114	93.66	U14003	(39819-39792)	ECD090.00	-
CP05115	CP05115	93.68	U14003	(40912-40885)	ECD090.00	-
CP05116	CP05116	93.72	U14003	(42672-42645)	ECD090.00	-
CP05117	CP05117	93.73	U14003	(43142-43170)	ECD090.00	-
CP05118	CP05118	93.79	U14003	(45667-45640)	ECD090.00	-
CP05119	CP05119	93.90	U14003	(51137-51110)	ECD090.00	-
CP05120	CP05120	93.94	U14003	(52808-52791)	ECD090.00	-
CP05121	CP05121	94.01	U14003	(55951-55924)	ECD090.00	-
CP05122	CP05122	94.05	U14003	(57814-57786)	ECD090.00	-
CP05123	CP05123	94.08	U14003	(59230-59203)	ECD090.00	-
CP05124	CP05124	94.09	U14003	(59507-59536)	ECD090.00	-
CP05125	CP05125	94.12	U14003	(61315-61344)	ECD090.00	-
CP05126	CP05126	94.21	U14003	(65199-65171)	ECD090.00	-
CP05127	CP05127	94.24	U14003	(66565-66537)	ECD090.00	-
CP05128	CP05128	94.31	U14003	(69866-69839)	ECD090.00	-
CP05129	CP05129	94.38	U14003	(73279-73252)	ECD090.00	-
CP05130	CP05130	94.38	U14003	(73410-73438)	ECD090.00	-
CP05131	CP05131	94.41	U14003	(74554-74583)	ECD090.00	-
CP05132	CP05132	94.53	U14003	(80245-80217)	ECD090.00	-
CP05133	CP05133	94.55	U14003	(81288-81260)	ECD090.00	-
CP05134	CP05134	94.58	U14003	(82270-82297)	ECD090.00	-
CP05135	CP05135	94.63	U14003	(84824-84840)	ECD090.00	-
CP05136	CP05136	94.63	U14003	(84955-84927)	ECD090.00	-
CP05137	CP05137	94.76	U14003	(91027-91054)	ECD090.00	-
CP05138	CP05138	94.85	U14003	(95106-95135)	ECD090.00	-
CP05139	CP05139	94.89	U14003	(96837-96866)	ECD090.00	-
CP05140	CP05140	94.97	U14003	(100809-100837)	ECD090.00	-
CP05141	CP05141	95.11	U14003	(107270-107242)	ECD090.00	-
CP05142	CP05142	95.16	U14003	(109285-109257)	ECD090.00	-
CP05143	CP05143	95.18	U14003	(110501-110472)	ECD090.00	-
CP05144	CP05144	95.19	U14003	(110739-110766)	ECD090.00	-
CP05145	CP05145	95.30	U14003	(115823-115851)	ECD090.00	-
CP05146	CP05146	95.35	U14003	(118355-118327)	ECD090.00	-

EP03730	CP03730	87.77	L19201	(37133-37161)	ECD085.00	-
EP03731	CP03731	87.85	L19201	(40642-40670)	ECD085.00	-
EP03732	CP03732	87.86	L19201	(41165-41194)	ECD085.00	-
EP03733	CP03733	88.00	L19201	(47579-47552)	ECD085.00	-
EP03734	CP03734	88.00	L19201	(47674-47701)	ECD085.00	-
EP03735	CP03735	88.02	L19201	(48522-48551)	ECD085.00	-
EP03736	CP03736	88.14	L19201	(54487-54461)	ECD085.00	-
EP03737	CP03737	88.14	L19201	(54505-54477)	ECD085.00	-
EP03738	CP03738	88.18	L19201	(56031-56003)	ECD085.00	-
EP03739	CP03739	88.24	L19201	(59140-59112)	ECD085.00	-
EP03740	CP03740	88.25	L19201	(59215-59186)	ECD085.00	-
EP03741	CP03741	88.25	L19201	(59347-59376)	ECD085.00	-
EP03742	CP03742	88.31	L19201	(62227-62198)	ECD085.00	-
EP03743	CP03743	88.31	L19201	(62358-62385)	ECD085.00	-
EP03744	CP03744	88.33	L19201	(63274-63302)	ECD085.00	-
EP03745	CP03745	88.36	L19201	(64316-64347)	ECD085.00	-
EP03746	CP03746	88.36	L19201	(64317-64345)	ECD085.00	-
EP03747	CP03747	88.42	L19201	(67337-67308)	ECD085.00	-
EP03748	CP03748	88.42	L19201	(67390-67419)	ECD085.00	-
EP03749	CP03749	88.44	L19201	(68037-68053)	ECD085.00	-
EP03750	CP03750	88.44	L19201	(68048-68075)	ECD085.00	-
EP03751	CP03751	88.46	L19201	(69069-69098)	ECD085.00	-
EP03752	CP03752	88.46	L19201	(69089-69105)	ECD085.00	-
EP03753	CP03753	88.49	L19201	(70382-70409)	ECD085.00	-
EP03754	CP03754	88.51	L19201	(71505-71532)	ECD085.00	-
EP03755	CP03755	88.55	L19201	(73238-73210)	ECD085.00	-
EP03756	CP03756	88.56	L19201	(73865-73893)	ECD085.00	-
EP03757	CP03757	88.56	L19201	(73906-73878)	ECD085.00	-
EP03758	CP03758	88.57	L19201	(74446-74475)	ECD085.00	-
EP03759	CP03759	88.69	L19201	(79829-79801)	ECD085.00	-
EP03760	CP03760	88.69	L19201	(80024-80052)	ECD085.00	-
EP03761	CP03761	88.71	L19201	(81025-80996)	ECD085.00	-
EP03762	CP03762	88.74	L19201	(82022-81993)	ECD085.00	-
EP03763	CP03763	88.78	L19201	(84019-83990)	ECD085.00	-
EP03764	CP03764	88.80	L19201	(85038-85010)	ECD085.00	-
EP03765	CP03765	88.82	L19201	(86148-86119)	ECD085.00	-
EP03766	CP03766	88.88	L19201	(88577-88550)	ECD085.00	-
EP03767	CP03767	88.88	L19201	(88557-88586)	ECD085.00	-
EP03768	CP03768	88.88	L19201	(88586-88557)	ECD085.00	-
EP03769	CP03769	88.90	L19201	(89533-89505)	ECD085.00	-
EP03770	CP03770	88.91	L19201	(90226-90197)	ECD085.00	-
EP03771	CP03771	88.91	L19201	(90233-90261)	ECD085.00	-
EP03772	CP03772	89.00	L19201	(94148-94176)	ECD085.00	-
EP03773	CP03773	89.02	L19201	(95410-95437)	ECD085.00	-
EP03776	CP03776	0.64	X70017	(118-144)	ECD000.00	-
EP03777	CP03777	0.64	X70017	(186-216)	ECD000.00	-
EP03779	CP03779	60.70	L07596	(682-708)	ECD060.00	-
EP03780	CP03780	27.98	M60918	(548-576)	ECD025.00	-
EP03781	CP03781	27.99	M60918	(792-821)	ECD025.00	-
EP04713	CP04713	17.51	M29632	(35-49)	ECD015.00	-
EP04714	CP04714	78.57	X80057	(655-683)	ECD075.00	-
EP04720	CP04720	93.66	X79886	(128-146)	ECD090.00	-
EP04725	CP04725	99.59	L27665	(32-72)	ECD095.00	-
EP04740	CP04740	39.10	J01615	(91-121)	ECD039.10	-
EP04741	CP04741	60.17	X65104	(136-149)	ECD060.00	-
lacP	CP00848	7.87	J01636	(1201-1275)	ECD005.00	-
lacP uv5	CP02815	7.87	K01793	(1-67)	ECD005.00	-
p-bglX	CP04882	47.84	U15049	(34-63)	ECD045.00	-
p-cls	CP04897	28.16	U15986	(77-104)	ECD025.00	-
p-cytRP	CP03782	88.83	X68638	(1-111)	ECD085.00	-

p-dsrA	CP05856	43.60	U17136	(865-893)	ECD040.00	-
p-fadL	CP03703	52.99	X70445	(1-166)	ECD050.00	-
p-fyuA	CP04888	-	Z38064	(74-101)	-	
p-hho	CP04893	72.80	U15661	(454-482)	ECD070.00	-
p-nfs	CP04879	13.03	D25414	(138-166)	ECD010.00	-
p-torR	CP04875	22.78	X78195	(2184-2156)	ECD020.00	-
pEnrR	CP05908	60.53	U19993	(255-283)	ECD060.00	-
pqi5B	CG06186	21.82	X81561	(2108-2382)	ECD020.00	-

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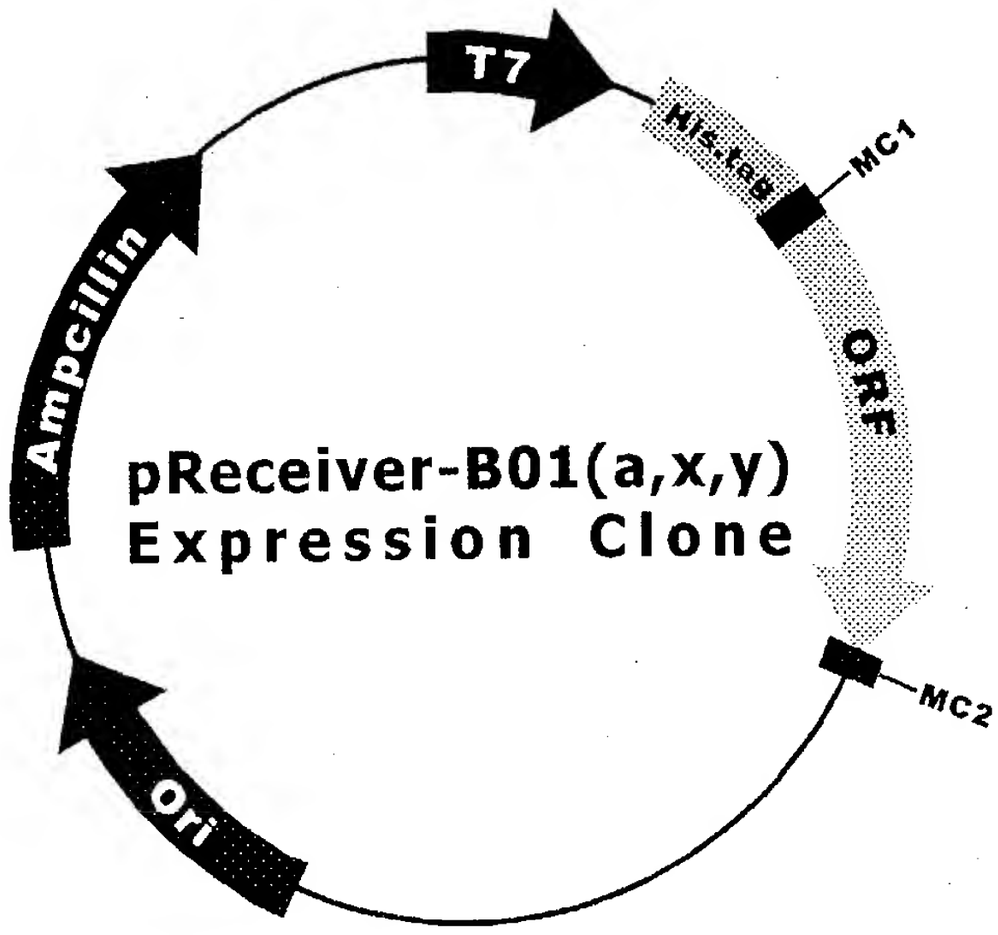
OmicsLink™ Clone (T7 Promoter)



pReceiver-B01a

T7 Promoter — rbs

TTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACATATG TCG

His.tag — Xmn I — ORF — Xho I — Not I

TAC TAC CAT CAC CAT CAC CAT CAT CAC GAA GGA GTT CGA ACC ATG.....TAGCTCGAGTGCGGCCGCA

Nsp V

pReceiver-B01x

T7 Promoter — rbs

TTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACATATG TCG

His.tag — Xmn I — Kpn I — ORF — Xho I — Not I

TAC TAC CAT CAC CAT CAC CAT CAT TCG AAG GAA TTC GGT ACC ATG.....TAGCTCGAGTGCGGCCGCA

EcoR I

pReceiver-B01y

T7 Promoter — rbs

TTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACATATG TCG

His.tag — ORF — Xho I — Not I

TAC TAC CAT CAC CAT CAC CAT CAT CAC GAA GGA ACC ACC ATG.....TAGCTCGAGTGCGGCCGCA

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Regulatory elements and transcriptional factors

For Yeast

Get factor & element list | Get consensus list | Get matrix list
Get distribution of mapped sites | Get summary of distribution
Get correlation between factors
Search none

Main

ABF1	TCRNNNNNNACG
ACE2	GCTGGT
ADR1	TCTCC
AP-1	TTANTAA
ATF	ACGTCA
BAS2	TAATRA
BAS2	TAANTAA
CPF1	TCACGTG
CuRE	GAGCAAA
CSRE	YCGGAYRRAWGG
SCB	CNCGAAA
GC/FAR	CCCGGG
GC/FAR	GGGCCC
GAL4	CGGNNNNNNNNNNCCG
GCN4	TGANTN
GCR1	CWTCC
HAP1	CGGNNNTANCGG
HSTF	GAANNTCC
HSTF	GAANNNTCC
HSTF	TTCNNGAA
HSTF	TTCNNNGAA
LEU3	CCGNNNNCGG or GGCNNNNGCC
MCB	WCGCGW
MCM1	CCNNNWWRGG
MATalpha2	CRTGTWWWW
MIG1	CCCCRNNWWWWW
MSE	CRCAAAW
NBF	ATGYGRAWW
PHO4	CACGTK
PDR3	TCCGYGGA
PPR1	TTCGGNNNNNNCCGAA
PUT3	CGGNNNNNNNNNNCCG
REB1	YYACCCG
ROX1	YYNATTGTTY
RAP1	RMACCCA
RME1	GAACCTCAA
repressor_of_CAR1	AGCCGCSA
SWI5	KGCTGR
STE12	TGAAACA
TBP	TATAWAW
T4C	TTTTCTYCG
TEA1	CGGNNNNNNNNNNCCG
UASPHR	CTTCCT
URSPHR	GTSAAAGTAWG

Regulatory elements

UASRAD	WTTTCCCGS
UASINO	ATGTGAAWW
SFF	GTMAACAA
ECB	GGAAAAD
STRE	AGGGG
ORC	WTTTATRTTTW

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CMV promoter sequence

TAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAAT
GGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACG
CCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAA
GTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAG
TACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATG
CGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATT
GACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCA
TTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAG

pBV-Luc Vector Map

pBV-Luc Vector Sequence